

What is claimed is:

Claim 1: Seed of maize inbred line designated G1704, representative seed of said line having been deposited under ATCC Accession No. PTA-XXXX.

Claim 2: A maize plant, or a part thereof, produced by growing the seed of claim 1.

Claim 3: The maize plant of claim 2 wherein said plant has been detasseled.

Claim 4: A tissue culture of regenerable cells produced from the plant of claim 2.

Claim 5: Protoplasts produced from the tissue culture of claim 4.

Claim 6: The tissue culture of claim 4, wherein cells of the tissue culture are from a tissue selected from the group consisting of leaf, pollen, embryo, root, root tip, anther, silk, flower, kernel, ear, cob, husk and stalk.

Claim 7: A maize plant regenerated from the tissue culture of claim 4, said plant having all the morphological and physiological characteristics of inbred line G1704, representative seed of said line having been deposited under ATCC Accession No. PTA XXXX.

Claim 8: A method for producing an F 1 hybrid maize seed, comprising crossing the plant of claim 2 with a different maize plant and harvesting the resultant F 1 hybrid maize seed.

Claim 9: A method of producing a male sterile maize plant comprising transforming the maize plant of claim 2 with a nucleic acid molecule that confers male sterility.

Claim 10: A male sterile maize plant produced by the method of claim 9.

Claim 11: A method of producing an herbicide resistant maize plant comprising transforming the maize plant of claim 2 with a transgene that confers herbicide resistance.

Claim 12: An herbicide resistant maize plant produced by the method of claim 11.

Claim 13: The maize plant of claim 12, wherein the transgene confers resistance to an herbicide selected from the group consisting of: imidazolinone, sulfonylurea, glyphosate, glufosinate, L-phosphinothricin, triazine and benzonitrile.

Claim 14: A method of producing an insect resistant maize plant comprising transforming the maize plant of claim 2 with a transgene that confers insect resistance.

Claim 15: An insect resistant maize plant produced by the method of claim 14.

Claim 16: The maize plant of claim 15, wherein the transgene encodes a *Bacillus thuringiensis* endotoxin.

Claim 17: A method of producing a disease resistant maize plant comprising transforming the maize plant of claim 2 with a transgene that confers disease resistance.

Claim 18: A disease resistant maize plant produced by the method of claim 17.

Claim 19: A method of producing a maize plant with decreased phytate content comprising transforming the maize plant of claim 2 with a transgene encoding phytase.

Claim 20: A maize plant with decreased phytate content produced by the method of claim 19.

Claim 21: A method of producing a maize plant with modified fatty acid metabolism

or modified carbohydrate metabolism comprising transforming the maize plant of claim 2 with a transgene encoding a protein selected from the group consisting of stearyl-ACP desaturase, fructosyltransferase, levansucrase, alpha-amylase, invertase and starch branching enzyme.

Claim 22: A maize plant produced by the method of claim 21.

Claim 23: The maize plant of claim 22 wherein the transgene confers a trait selected from the group consisting of waxy starch and increased amylose starch.

Claim 24: A maize plant, or part thereof, having all the physiological and morphological characteristics of the inbred line G1704, representative seed of said line having been deposited under ATCC Accession No. PTA-XXXX.

Claim 25: A method of introducing a desired trait into maize inbred line G1704 comprising:

(a) crossing G1704 plants grown from G1704 seed, representative seed of which has been deposited under ATCC Accession No. PTA-XXXX, with plants of another maize line that comprise a desired trait to produce F 1 progeny plants, wherein the desired trait is selected from the group consisting of male sterility, herbicide resistance, insect resistance, disease resistance and waxy starch;

(b) selecting F 1 progeny plants that have the desired trait to produce selected F 1 progeny plants;

(c) crossing the selected progeny plants with the G1704 plants to produce backcross progeny plants;

(d) selecting for backcross progeny plants that have the desired trait and physiological and morphological characteristics of maize inbred line G1704 listed in Table 1 to produce selected backcross progeny plants; and

(e) repeating steps (c) and (d) three or more times in succession to produce selected fourth or higher backcross progeny plants that comprise the desired trait and all of the physiological and morphological characteristics of maize inbred line G1704

listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions.

Claim 26: A plant produced by the method of claim 25, wherein the plant has the desired trait and all of the physiological and morphological characteristics of maize inbred line G1704 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions.

Claim 27: The plant of claim 26 wherein the desired trait is herbicide resistance and the resistance is conferred to an herbicide selected from the group consisting of: imidazolinone, sulfonylurea, glyphosate, glufosinate, L-phosphinothricin, triazine and benzonitrile.

Claim 28: The plant of claim 26 wherein the desired trait is insect resistance and the insect resistance is conferred by a transgene encoding a *Bacillus thuringiensis* endotoxin.

Claim 29: The plant of claim 26 wherein the desired trait is male sterility and the trait is conferred by a cytoplasmic nucleic acid molecule that confers male sterility.

Claim 30: A method of modifying fatty acid metabolism, modified phytic acid metabolism or modified carbohydrate metabolism into maize inbred line G1704 comprising:

(a) crossing G1704 plants grown from G1704 seed, representative seed of which has been deposited under ATCC Accession No. PTA-XXXX, with plants of another maize line that comprise a nucleic acid molecule encoding an enzyme selected from the group consisting of phytase, stearyl-ACP desaturase, fructosyltransferase, levansucrase, alphaamylase, invertase and starch branching enzyme;

(b) selecting F 1 progeny plants that have said nucleic acid molecule to produce selected F 1 progeny plants;

(c) crossing the selected progeny plants with the G1704 plants to produce

backcross progeny plants;

(d) selecting for backcross progeny plants that have said nucleic acid molecule and physiological and morphological characteristics of maize inbred line G1704 listed in Table 1 to produce selected backcross progeny plants; and

(e) repeating steps (c) and (d) three or more times in succession to produce selected fourth or higher backcross progeny plants that comprise said nucleic acid molecule and have all of the physiological and morphological characteristics of maize inbred line G1704 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions.

Claim 31: A plant produced by the method of claim 30, wherein the plant comprises the nucleic acid molecule and has all of the physiological and morphological characteristics of maize inbred line G1704 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions.